

# SEQUENCE LISTING

<110> Tsuji, Takashi  
Tezuka, Katsunari  
Hori, Nobuaki

<120> HUMAN MONOCLONAL ANTIBODY AGAINST A  
COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND  
PHARMACEUTICAL USE THEREOF

<130> 06501-079001

<140> US 09/859,053

<141> 2001-05-16

<150> JP 2001-99508

<151> 2001-03-30

<150> JP 2000-147116

<151> 2000-05-18

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21

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21

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	Met	Asp	Trp	Thr	Trp	Arg Ile Leu Phe Leu Val Ala Ala Ala	
	-5					-10	
aca gga gcc	cac tcc	cag gtg	cag ctg	gtg cag	tct ggg	gct gag gtg	158
Thr Gly Ala	His Ser	Gln Val	Gln Leu	Val Gln	Ser Gly	Ala Glu Val	
-5		1		5		10	
aag aag cct	ggg gcc	tca gtg	aag gtc	tcc tgc	aag gct	tct gga tac	206
Lys Lys Pro	Gly Ala	Ser Val	Lys Val	Ser Cys	Lys Ala	Ser Gly Tyr	
	15		20		25		
acc ttc acc	ggc tac	tat atg	cac tgg	gtg cga	cag gcc	cct gga caa	254
Thr Phe Thr	Gly Tyr	Tyr Met	His Trp	Val Arg	Gln Ala	Pro Gly Gln	
	30		35		40		
ggg ctt gag	tgg atg	gga tgg	atc aac	cct cac	agt ggt	ggc aca aac	302
Gly Leu Glu	Trp Met	Gly Trp	Ile Asn	Pro His	Ser Gly	Gly Thr Asn	
	45		50		55		
tat gca cag	aag ttt	cag ggc	agg gtc	acc atg	acc agg	gac acg tcc	350
Tyr Ala Gln	Lys Phe	Gln Gly	Arg Val	Thr Met	Thr Arg	Asp Thr Ser	
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atc agc aca	gcc tac	atg gag	ctg agc	agg ctg	aga tcc	gac gac acg	398
Ile Ser Thr	Ala Tyr	Met Glu	Leu Ser	Arg Leu	Arg Ser	Asp Asp Thr	
	80		85		90		
gcc gtg tat	tac tgt	gcg agg	acg tat	tac tat	gat agt	agt ggt tat	446
Ala Val Tyr	Tyr Cys	Ala Arg	Thr Tyr	Tyr Tyr	Asp Ser	Ser Gly Tyr	
	95		100		105		
tac cat gat	gct ttt	gat atc	tgg ggc	caa ggg	aca atg	gtc acc gtc	494
Tyr His Asp	Ala Phe	Asp Ile	Trp Gly	Gln Gly	Thr Met	Val Thr Val	
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tct tca gcc	tcc acc	aag ggc	cca tcg	gtc ttc	ccc ctg	gcg ccc tgc	542
Ser Ser Ala	Ser Thr	Lys Gly	Pro Ser	Val Phe	Pro Leu	Ala Pro Cys	
	125		130		135		
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Ser Arg Ser	Thr Ser	Glu Ser	Thr Ala	Ala Leu	Gly Cys	Leu Val Lys	
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gac tac ttc	ccc gaa	ccg gtg	acg gtg	tcg tgg	aac tca	ggc gct ctg	638
Asp Tyr Phe	Pro Glu	Pro Val	Thr Val	Ser Trp	Asn Ser	Gly Ala Leu	
	160		165			170	
acc agc ggc	gtg cac	acc ttc	cca gct	gtc cta	cag tcc	tca gga ctc	686
Thr Ser Gly	Val His	Thr Phe	Pro Ala	Val Leu	Gln Ser	Ser Gly Leu	
	175		180			185	



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gac aag aca gtt gag cgc aaa tgt tgt gtc gag tgc cca ccg tgc cca Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro 220 225 230 235	830
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aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc gtg gtg Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val 255 260 265	926
gtg gac gtg agc cac gaa gac ccc gag gtc cag ttc aac tgg tac gtg Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val 270 275 280	974
gac ggc gtg gag gtg cat aat gcc aag aca aag cca cgg gag gag cag Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln 285 290 295	1022
ttc aac agc acg ttc cgt gtg gtc agc gtc ctc acc gtt gtg cac cag Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln 300 305 310 315	1070
gac tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac aaa ggc Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly 320 325 330	1118
ctc cca gcc ccc atc gag aaa acc atc tcc aaa acc aaa ggg cag ccc Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro 335 340 345	1166
cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr 350 355 360	1214
aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser 365 370 375	1262
gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr 380 385 390 395	1310
aag acc aca cct ccc atg ctg gac tcc gac ggc tcc ttc ttc ctc tac Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr 400 405 410	1358
agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc	1406

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  
 415 420 425

tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag 1454  
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
 430 435 440

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 Ser Leu Ser Leu Ser Pro Gly Lys  
 445 450

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 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 50 55 60  
 Glu Trp Met Gly Trp Ile Asn Pro His Ser Gly Gly Thr Asn Tyr Ala  
 65 70 75 80  
 Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser  
 85 90 95  
 Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val  
 100 105 110  
 Tyr Tyr Cys Ala Arg Thr Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr His  
 115 120 125  
 Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser  
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 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
 145 150 155 160  
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 165 170 175  
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 180 185 190  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 195 200 205  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr  
 210 215 220  
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 225 230 235 240  
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245 250 255  
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 260 265 270  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 275 280 285  
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly

290		295		300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn				
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Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp				
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Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro				
	340		345	350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu				
	355		360	365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn				
	370		375	380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile				
385		390		395
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr				
	405		410	415
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys				
	420		425	430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys				
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Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu				
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Ser Leu Ser Pro Gly Lys				
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 Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Phe Pro Gly Ser Arg Cys  
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gac atc cag atg acc cag tct cca tct tcc gtg tct gca tct gta gga 152  
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
 1 5 10 15

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 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Arg Leu

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tat gtt gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agc ggc Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly 50 55 60			296
agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro 65 70 75 80			344
gaa gat ttt gca act tac tat tgt caa cag gct aac agt ttc ccg tgg Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Trp 85 90 95			392
acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala 100 105 110			440
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly 115 120 125			488
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala 130 135 140			536
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln 145 150 155 160			584
gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser 165 170 175			632
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr 180 185 190			680
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser 195 200 205			728
ttc aac agg gga gag tgt tagagggaga agtgccccc cctgctcctc Phe Asn Arg Gly Glu Cys 210			776
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&lt;210&gt; 30

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

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          20           25           30
Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
          35           40           45
Gln Gly Ile Ser Arg Leu Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
          50           55           60
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
65           70           75           80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
          85           90           95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
          100          105          110
Ala Asn Ser Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
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Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
          130          135          140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145          150          155          160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
          165          170          175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
          180          185          190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
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Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
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&lt;210&gt; 31

&lt;211&gt; 1708

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; 5'UTR

&lt;222&gt; (1)...(93)

&lt;221&gt; CDS

&lt;222&gt; (94)...(1503)

&lt;221&gt; 3'UTR

&lt;222&gt; (1507)...(1708)

&lt;221&gt; sig\_peptide

&lt;222&gt; (94)...(150)

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1708)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 31

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 Met Glu Leu Gly Leu Ser Trp

-15

gtt ttc ctt gtt gct ata tta gaa ggt gtc cag tgt gag gtg cag ctg 162  
 Val Phe Leu Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln Leu  
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gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc ctg aga ctc 210  
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 5 10 15 20

tcc tgt gca gcc tct gga ttc acc ttc agt agc tac gac atg cac tgg 258  
 Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met His Trp  
 25 30 35

gtc cgc caa gct aca gga aaa ggt ctg gag tgg gtc tca gct att ggt 306  
 Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Gly  
 40 45 50

act gct ggt gac aca tac tat cca ggc tcc gtg aag ggc cga ttc acc 354  
 Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys Gly Arg Phe Thr  
 55 60 65

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 70 75 80

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 85 90 95 100

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 Lys Val Thr His Glu His Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly  
 105 110 115

caa ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg 546  
 Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 120 125 130

gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca gcg 594  
 Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala  
 135 140 145

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 642  
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 150 155 160

tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca gct 690  
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 165 170 175 180

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 738  
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 185 190 195

ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat cac Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His 200 205 210	786
aag ccc agc aac acc aag gtg gac aag aca gtt gag cgc aaa tgt tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys 215 220 225	834
gtc gag tgc cca ccg tgc cca gca cca cct gtg gca gga ccg tca gtc Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val 230 235 240	882
ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr 245 250 255 260	930
cct gag gtc acg tgc gtg gtg gtg gac gtg agc cac gaa gac ccc gag Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu 265 270 275	978
gtc cag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys 280 285 290	1026
aca aag cca cgg gag gag cag ttc aac agc acg ttc cgt gtg gtc agc Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser 295 300 305	1074
gtc ctc acc gtt gtg cac cag gac tgg ctg aac ggc aag gag tac aag Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys 310 315 320	1122
tgc aag gtc tcc aac aaa ggc ctc cca gcc ccc atc gag aaa acc atc Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile 325 330 335 340	1170
tcc aaa acc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro 345 350 355	1218
cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu 360 365 370	1266
gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc aat Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn 375 380 385	1314
ggg cag ccg gag aac aac tac aag acc aca cct ccc atg ctg gac tcc Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser 390 395 400	1362
gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg 405 410 415 420	1410

tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg 1458  
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
                   425                  430                  435

cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa 1503  
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
                   440                  445                  450

tgagtgccac ggccggcaag cccccgctcc ccaggctctc ggggtcgcgt gaggatgctt 1563  
 ggcacgtacc ccgtgtacat acttcccagg caccagcat ggaaataaag caccagcgc 1623  
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 aaaaaaaaaa aatctctgcg gccgc 1708

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                   20                  25                  30  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
                   35                  40                  45  
 Ser Ser Tyr Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu  
   50                  55                  60  
 Glu Trp Val Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly  
 65                  70                  75                  80  
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser  
                   85                  90                  95  
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr  
                   100                  105                  110  
 Tyr Cys Val Arg Asp Asn Arg Lys Val Thr His Glu His Tyr Tyr Tyr  
                   115                  120                  125  
 Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
                   130                  135                  140  
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
 145                  150                  155                  160  
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
                   165                  170                  175  
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
                   180                  185                  190  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
                   195                  200                  205  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr  
                   210                  215                  220  
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 225                  230                  235                  240  
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
                   245                  250                  255  
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
                   260                  265                  270  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
                   275                  280                  285  
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly  
                   290                  295                  300



Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn  
 305 310 315 320  
 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp  
 325 330 335  
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro  
 340 345 350  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu  
 355 360 365  
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 370 375 380  
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 385 390 395 400  
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 405 410 415  
 Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 420 425 430  
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 435 440 445  
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
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 Ser Leu Ser Pro Gly Lys  
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 <222> (28)...(735)

<221> 3'UTR  
 <222> (739)...(948)

<221> sig\_peptide  
 <222> (28)...(87)

<221> misc\_feature  
 <222> (1)...(948)  
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ctc ctg cta ctc tgg ctc cca gat acc acc gga gaa att gtg ttg acg 102  
 Leu Leu Leu Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val Leu Thr  
 -10 -5 1 5

cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc 150  
 Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu  
 10 15 20

tcc tgc agg gcc agt cag aat att aga agc agc tac tta gcc tgg tac	198
Ser Cys Arg Ala Ser Gln Asn Ile Arg Ser Ser Tyr Leu Ala Trp Tyr	
25 30 35	
cag cag aaa cct ggc cag gct ccc ggg ctc ctc atc tat ggt gca tcc	246
Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu Ile Tyr Gly Ala Ser	
40 45 50	
agc agg gcc act ggc atc cca gac agg ttc agt ggc agt ggg tct ggg	294
Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly	
55 60 65	
aca gac ttc act ctc acc atc agc aga ctg gag cct gaa gat ttt gca	342
Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala	
70 75 80 85	
gtg tat tac tgt cag cag ttt ggt agc tca cct atg tgc agt ttt ggc	390
Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro Met Cys Ser Phe Gly	
90 95 100	
cag ggg acc aag ctg gag atc aaa cga act gtg gct gca cca tct gtc	438
Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val	
105 110 115	
ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct	486
Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser	
120 125 130	
gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag	534
Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln	
135 140 145	
tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc	582
Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val	
150 155 160 165	
aca gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg	630
Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu	
170 175 180	
acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa	678
Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu	
185 190 195	
gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg	726
Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg	
200 205 210	
gga gag tgt tagagggaga antgccccca cctgtctctc agttccagcc	775
Gly Glu Cys	
215	
tgacccccctc ccatacctttg gcctctgacc ctttttccac aggggaccta cccctattgc	835
ggctctccag ctcactcttc acctaccccc cctcctctc cttggcttta attatgctaa	895
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           20                  25                  30  
 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asn  
           35                  40                  45  
 Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
           50                  55                  60  
 Pro Gly Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro  
   65                  70                  75                  80  
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
           85                  90                  95  
 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe  
          100                 105                 110  
 Gly Ser Ser Pro Met Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile  
          115                 120                 125  
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
          130                 135                 140  
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
  145                 150                 155                 160  
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
          165                 170                 175  
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
          180                 185                 190  
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
          195                 200                 205  
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
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Met Glu Leu Gly Leu Ser	
-15	
tggtgtttttctt gtt gct ata tta gaa ggt gtc cag tgt gag gtg cag	161
Trp Val Phe Leu Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln	
-10 -5 1	
ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc ctg aga	209
Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg	
5 10 15	
ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tac gac atg cac	257
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met His	
20 25 30 35	
tggtgtc cgc caa gct aca gga aaa ggt ctg gag tgg gtc tca gct att	305
Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val Ser Ala Ile	
40 45 50	
ggt act gct ggt gac aca tac tat cca ggc tcc gtg aag ggc cga ttc	353
Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys Gly Arg Phe	
55 60 65	
acc atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt caa atg aac	401
Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn	
70 75 80	
agc ctg aga gcc ggg gac acg gct gtg tat tac tgt gta aga gat aag	449
Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Lys	
85 90 95	
agg acg gtg acc cac gag cac tac tac tac tac ggt atg gac gtc tgg	497
Arg Thr Val Thr His Glu His Tyr Tyr Tyr Tyr Gly Met Asp Val Trp	
100 105 110 115	
ggc caa ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca	545
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	
120 125 130	
tcg gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca	593
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr	
135 140 145	
gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acc	641
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr	
150 155 160	
gtg tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca	689
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro	
165 170 175	
gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc	737
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr	
180 185 190 195	
gtg ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat	785

Val	Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	Asp		
				200					205					210			
cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aca	gtt	gag	cgc	aaa	tgt	833	
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Arg	Lys	Cys		
			215					220					225				
tgt	gtc	gag	tgc	cca	ccg	tgc	cca	gca	cca	cct	gtg	gca	gga	ccg	tca	881	
Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser		
		230					235					240					
gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	929	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg		
	245					250					255						
acc	cct	gag	gtc	acg	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	ccc	977	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro		
260					265				270						275		
gag	gtc	cag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	1025	
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala		
				280					285					290			
aag	aca	aag	cca	cgg	gag	gag	cag	ttc	aac	agc	acg	ttc	cgt	gtg	gtc	1073	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val		
			295					300					305				
agc	gtc	ctc	acc	gtt	gtg	cac	cag	gac	tgg	ctg	aac	ggc	aag	gag	tac	1121	
Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr		
		310					315					320					
aag	tgc	aag	gtc	tcc	aac	aaa	ggc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	1169	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr		
	325					330					335						
atc	tcc	aaa	acc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	1217	
Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu		
340					345					350					355		
ccc	cca	tcc	cgg	gag	gag	atg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	1265	
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys		
				360					365					370			
ctg	gtc	aaa	ggc	ttc	tac	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	1313	
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser		
			375					380					385				
aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	aca	cct	ccc	atg	ctg	gac	1361	
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp		
			390				395					400					
tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	1409	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser		
	405					410					415						
agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	1457	
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala		

420                      425                      430                      435                      1505  
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 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
                     440                      445                      450

tgagtgccac ggccggcaag cccccgctcc ccaggctctc ggggtcgcgt gaggatgctt 1565  
 ggacagtacc ccgtgtacat acttcccagg caccagcat ggaaataaag caccagcgc 1625  
 tgccctgggc ccctgcgaaa aaaaaaaaaa aaaaatctct gcggccgc 1673

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 <213> Homo sapiens

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                     20                    25                    30  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
                     35                    40                    45  
 Ser Ser Tyr Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu  
                     50                    55                    60  
 Glu Trp Val Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly  
   65                    70                    75                    80  
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser  
                     85                    90                    95  
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr  
                     100                    105                    110  
 Tyr Cys Val Arg Asp Lys Arg Thr Val Thr His Glu His Tyr Tyr Tyr  
                     115                    120                    125  
 Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
                     130                    135                    140  
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
   145                    150                    155                    160  
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
                     165                    170                    175  
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
                     180                    185                    190  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
                     195                    200                    205  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr  
                     210                    215                    220  
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
   225                    230                    235                    240  
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
                     245                    250                    255  
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
                     260                    265                    270  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
                     275                    280                    285  
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly  
                     290                    295                    300  
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn  
   305                    310                    315                    320  
 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp

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          325          330          335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
          340          345          350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
          355          360          365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
          370          375          380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
          385          390          395          400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
          405          410          415
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
          420          425          430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
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Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
          450          455          460
Ser Leu Ser Pro Gly Lys
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<212> DNA
<213> Homo sapiens

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<220>
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<221> 3'UTR
<222> (744)...(970)

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<221> sig_peptide
<222> (33)...(92)

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<400> 37
gaattcgag tgccatgaca ccacgggggaa cc atg gaa acc cca ggc cag ctt      53
                               Met Glu Thr Pro Ala Gln Leu
                               -20                               -15

ctc ttc ctc ctg cta ctc tgg ctc cca gat acc acc gga gaa att gtg      101
Leu Phe Leu Leu Leu Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val
                               -10                               -5                               1

ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc      149
Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
          5          10          15

acc ctc tcc tgc agg gcc agt cag agt att agc agc agc tcc tta gcc      197
Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Ser Ser Ser Leu Ala
          20          25          30          35

tgg tac cag cag aaa cct ggc cag gct ccc ggg ctc ctc atc ttt ggt      245
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu Ile Phe Gly

```

40	45	50	
gca tcc agc agg gcc act ggc atc cca gac agg ttc agt ggc agt ggg			293
Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly			
55	60	65	
tct ggg aca gac ttc act ctg acc atc agc aga ctg gag cct gaa gat			341
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp			
70	75	80	
ttt gca gtg tat tac tgt cag cag ttt ggt agc tca cct atg tgc agt			389
Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro Met Cys Ser			
85	90	95	
ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg gct gca cca			437
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro			
100	105	110	115
tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act			485
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr			
120	125	130	
gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa			533
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys			
135	140	145	
gta cag tgg aag gtg gat aac gcc ctg caa tgg ggt aac tcc cag gag			581
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu			
150	155	160	
agt gtc aca gag cag gac agc aag gac agc acc tac agc ctg agc agc			629
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser			
165	170	175	
acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc			677
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala			
180	185	190	195
tgc gaa gtc acc cat cag ggc ctg agc tgg ccc gtc aca aag agc ttc			725
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe			
200	205	210	
aac agg gga gag tgt tagagggaga agtgccccc cctgctcctc agttccagcc			780
Asn Arg Gly Glu Cys			
215			
tgacccccctc ccatacctttg gcctctgacc ctttttccac aggggaccta cccctattgc			840
ggctcctccag ctcatctttc acctcaccac cctcctcctc cttggcttta attatgctaa			900
tgattggagga gaatgaataa ataaagtga tctttgcaaa aaaaaaaaaa aaaaaaatct			960
ctgcggccgc			970

&lt;210&gt; 38

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 38



Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro  
 1 5 10 15  
 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser  
 20 25 30  
 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser  
 35 40 45  
 Ile Ser Ser Ser Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
 50 55 60  
 Pro Gly Leu Leu Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro  
 65 70 75 80  
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
 85 90 95  
 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe  
 100 105 110  
 Gly Ser Ser Pro Met Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile  
 115 120 125  
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 130 135 140  
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 145 150 155 160  
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
 165 170 175  
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
 180 185 190  
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
 195 200 205  
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
 210 215 220  
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

<210> 39

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized primer sequence

<221> primer\_bind

<222> (1)...(35)

<400> 39

gaggtctccg ccctcgagat gcggtgggc agtcc

35

<210> 40

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized primer sequence

<221> primer\_bind

<222> (1)...(33)

<400> 40

cacaggacag ccaggggatc ccacgtggcc gcg

33

<210> 41

<211> 6

<212> PRT

<213> Homo sapiens

<400> 41

Met Tyr Pro Pro Pro Tyr

1

5

<210> 42

<211> 4

<212> PRT

<213> Homo sapiens

<400> 42

Tyr Met Asn Met

1

<210> 43

<211> 4

<212> PRT

<213> Homo sapiens

<400> 43

Tyr Val Lys Met

1